AMENDMENTS TO THE SPECIFICATION

Please replace paragraph [0012] with the following amended paragraph:

[0012] In other preferred embodiments, comparative protein profiles are generated using the ProteinChip® Biomarker System from patients diagnosed with prostate cancer and from patients without known neoplastic diseases. A subset of biomarkers was selected based on collaborative results from supervised analytical methods. Preferred analytical methods include the Classification And Regression Tree (CART), implemented in Biomarker Pattern Software V4.0 (BPS) (Ciphergen, Calif.), and the Unified Maximum Separability Analysis (UMSA) procedure, implemented in ProPeak (3Z Informatics, SC).

Please replace paragraph [0466] with the following amended paragraph:

[0466] In a preferred embodiment, a serum sample is collected from a patient and then fractionated using an anion exchange resin as described above. The biomarkers in the sample are captured using an IMAC3 nickel ProteinChip® array. The markers are then detected using SELDI. The results are then entered into a computer system, which contains an algorithm that is designed using the same parameters that were used in the learning algorithm and classification algorithm to originally determine the biomarkers. The algorithm produces a diagnosis based upon the data received relating to each biomarker.

Please replace paragraph [0468] with the following amended paragraph:

[0468] In another embodiment, the sample is collected from the patient. The biomarkers are captured using an antibody ProteinChip® array as described above. The markers are detected using a biospecific SELDI test system. The results are then entered into a computer system, which contains an algorithm that is designed using the same parameters that were used in the learning algorithm and classification algorithm

to originally determine the biomarkers. The algorithm produces a diagnosis based upon the data received relating to each biomarker.